

SEQUENCE LISTING

(1)

GENERAL INFORMATION:

- (i) APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
- (ii) TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fulbright & Jaworski L.L.P.
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/906,068
(B) FILING DATE: July 11, 2001
- (vii) PRIOR APPLICATION DATE:
(A) APPLICATION NUMBER: 08/436,265
(B) FILING DATE: October 30, 1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/GB93/02367
(B) FILING DATE: November 17, 1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9224057.1
(B) FILING DATE: November 17, 1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304677.9
(B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304680.3
(B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9311047.6
(B) FILING DATE: May 28, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 9313763.6
(B) FILING DATE: July 2, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 9316099.2
(B) FILING DATE: August 3, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 321344.5
(B) FILING DATE: October 15, 1993

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Norman D. Hanson
(B) REGISTRATION NUMBER: 30,946
(C) REFERENCE/DOCKET NUMBER: LUD 5298.4 DIV (10105901)

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 318-3000
(B) TELEFAX: (212) 318-3400

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA      60
AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC      120
GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCCGACCCC AGCCCCCCGT      180
CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA      240
AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC      294
                               Met Thr Leu Gly
                               1
TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG      342
Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
   5              10              15              20
GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT      390
Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
              25              30              35
GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA      438
Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
              40              45              50
GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC      486
Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
              55              60              65
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TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC 534
Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
70 75 80
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC 582
Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
85 90 95 100
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT 630
Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp
105 110 115
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG 678
Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu
120 125 130
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG 726
Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu
135 140 145
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG 774
Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu
150 155 160
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT 822
Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser
165 170 175 180
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870
Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg
185 190 195
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918
Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg
200 205 210
TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC 966
Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val
215 220 225
AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG 1014
Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu
230 235 240
ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC 1062
Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile
245 250 255 260
GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC 1110
Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile
265 270 275
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG 1158
Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln
280 285 290
ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC 1206
Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys
295 300 305
GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA 1254
Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro
310 315 320
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC 1302
Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser
325 330 335 340
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA 1350
Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser
345 350 355
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC 1398
Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr
360 365 370

AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC 1446
 Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
 375 380 385
 TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG 1494
 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
 390 395 400
 CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC 1542
 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
 405 410 415 420
 TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG 1590
 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
 425 430 435
 GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT 1638
 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
 440 445 450
 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG 1686
 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
 455 460 465
 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG 1734
 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
 470 475 480
 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA 1782
 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
 485 490 495 500
 GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC 1831
 Val Ile Gln

 TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG 1891
 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT 1951
 ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA 1984

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
 1 5 10 15
 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
 20 25 30
 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
 35 40 45
 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
 50 55 60
 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
 65 70 75 80
 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
 85 90 95
 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
 100 105 110
 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
 115 120 125
 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
 130 135 140

Arg	Arg	Gln	Glu	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser
145					150					155					160
Ser	Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp
				165					170						175
Leu	Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe
			180					185						190	
Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val
		195					200					205			
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu
	210					215					220				
Ser	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe
225				230						235					240
Arg	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile
			245						250					255	
Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln
			260					265						270	
Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe
	275						280					285			
Leu	Gln	Arg	Gln	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val
	290					295					300				
Ser	Ala	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr
305				310						315					320
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val
			325						330					335	
Leu	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
		340						345					350		
Val	Met	His	Ser	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro
	355						360					365			
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Gln
	370					375					380				
Ile	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala
385				390						395					400
Phe	Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Val	Asn	Gly
			405						410					415	
Ile	Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Val	Val	Pro	Asn	Asp
		420						425					430		
Pro	Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr
	435						440					445			
Pro	Thr	Ile	Pro	Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu
	450					455					460				
Ala	Gln	Met	Met	Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu
465				470						475					480
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Gln	Lys	Ile	Ser	Asn	Ser	Pro
			485						490					495	
Glu	Lys	Pro	Lys	Val	Ile	Gln									
			500												

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG      60
GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA      115
                               Met Val Asp Gly
                               1
GTG ATG ATT CTT CTT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT      163
Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
   5                10                15                20
ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG      211
Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
                25                30                35
TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG      259
Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
                40                45                50
TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA      307
Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
                55                60                65
GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG      355
Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
                70                75                80
CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC      403
Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
                85                90                95                100
AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA      451
Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
                105                110                115
ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG      499
Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
                120                125                130
TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA      547
Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
                135                140                145
TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT      595
Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
                150                155                160
GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA      643
Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
                165                170                175                180
GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT      691
Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
                185                190                195
CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG      739
Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
                200                205                210
TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA      787
Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln
                215                220                225
GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA      835
Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser
                230                235                240
TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA      883
Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu
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245	AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT	250	Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser	255	260	931
	265	270	275			
ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC	979	Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr				
	280	285	290			
GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA	1027	Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile				
	295	300	305			
GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT	1075	Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe				
	310	315	320			
GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA	1123	Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys				
	325	330	335	340		
AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC	1171	Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly				
	345	350	355			
CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC	1219	Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn				
	360	365	370			
AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT	1267	Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp				
	375	380	385			
GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT	1315	Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile				
	390	395	400			
TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC	1363	Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser				
	405	410	415	420		
AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC	1411	Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro				
	425	430	435			
AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA	1459	Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln				
	440	445	450			
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC	1507	Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr				
	455	460	465			
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA	1555	Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala				
	470	475	480			
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT	1603	Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn				
	485	490	495	500		
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTC	1650	Ser Leu Asp Lys Leu Lys Thr Asp Cys				
	505					
GAAGGAAGAT TTGACGTTGT TGTCAATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT	1710					
TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC	1770					
GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA	1830					
ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA	1890					
AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG	1950					
GCTTTGCATA GCTTTACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT	2010					
GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG GAATTCCTTG	2070					
CATTCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT	2130					

GCGTACTCCA	CTGGTCTGTC	TTTGGATAAT	AGGAATTCAA	TTTGGCAAAA	CAAAATGTAA	2190
TGTCAGACTT	TGCTGCATTT	TACACATGTG	CTGATGTTTA	CAATGATGCC	GAACATTAGG	2250
AATTGTTTAT	ACACAACTTT	GCAAATTATT	TATTACTTGT	GCACTTAGTA	GTTTTTACAA	2310
AACTGCTTTG	TGCATATGTT	AAAGCTTATT	TTTATGTGGT	CTTATGATTT	TATTACAGAA	2370
ATGTTTTTAA	CACTATACTC	TAAAATGGAC	ATTTTCTTTT	ATTATCAGTT	AAAATCACAT	2430
TTTAAGTGCT	TCACATTTGT	ATGTGTGTAG	ACTGTAACCT	TTTTTCAGTT	CATATGCAGA	2490
ACGTATTTAG	CCATTACCCA	CGTGACACCA	CCGAATATAT	TATCGATTTA	GAAGCAAAGA	2550
TTTCAGTAGA	ATTTTAGTCC	TGAACGCTAC	GGGGAAAATG	CATTTTCTTC	AGAATTATCC	2610
ATTACGTGCA	TTTAAACTCT	GCCAGAAAAA	AATAACTATT	TTGTTTTAAT	CTACTTTTGT	2670
TATTTAGTAG	TTATTTGTAT	AAATTAAATA	AACTGTTTTT	AAGTCAAAAA	AAAA	2724

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Asp	Gly	Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala	Leu	1	5	10	15
Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro	Lys	Leu	20	25	30	
Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys	35	40	45	
Glu	Gly	Gln	Gln	Cys	Phe	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His		50	55	60	
Val	Tyr	Gln	Lys	Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr	65	70	75	80
Cys	Lys	Thr	Pro	Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly	85	90	95	
Asp	Trp	Cys	Asn	Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys	100	105	110	
Ser	Phe	Pro	Gly	Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile	115	120	125	
Leu	Ser	Val	Val	Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val	130	135	140	
Ala	Leu	Arg	Lys	Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg	145	150	155	160
Asp	Val	Glu	Tyr	Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly	165	170	175	
Asp	Ser	Thr	Leu	Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser	180	185	190	
Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile	195	200	205	
Thr	Leu	Leu	Glu	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	210	215	220	
Gly	Ser	Trp	Gln	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	225	230	235	240
Asp	Glu	Lys	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met	245	250	255	
Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	260	265	270	
Arg	His	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met	275	280	285	
Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser	290	295	300	

Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
 305 310 315 320
 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
 325 330 335
 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
 340 345 350
 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
 355 360 365
 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
 370 375 380
 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
 385 390 395 400
 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
 405 410 415
 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
 420 425 430
 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
 435 440 445
 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
 450 455 460
 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
 465 470 475 480
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
 485 490 495
 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
 500 505

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT	60
CAGTTTAATA CTGTCTTGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA	120
AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG	180
TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA	240
TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC	300
AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC	348
Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala	
1 5 10	
TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG	396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met	
15 20 25	
CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA	444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu	

30	AAT GGA GTA ACC TTA	35	GCA CCA GAG GAT ACC	40	TTG CCT TTT TTA	45	AAG TGC	492
	Asn Gly Val Thr		Leu Ala Pro Glu Asp Thr		Leu Pro Phe Leu		Lys Cys	
		50		55		60		
TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA	540							
Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile								
	65		70		75			
ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA	588							
Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu								
	80		85		90			
ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG	636							
Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln								
	95		100		105			
TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT	684							
Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys								
	110		115		120		125	
CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT	732							
Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val								
	130		135		140			
GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC	780							
Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu								
	145		150		155			
ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC	828							
Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys								
	160		165		170			
TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC	876							
Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr								
	175		180		185			
AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA	924							
Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser								
	190		195		200		205	
CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA	972							
Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly								
	210		215		220			
CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC	1020							
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val								
	225		230		235			
CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG	1068							
Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp								
	240		245		250			
CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC	1116							
Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala								
	255		260		265			
AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT	1164							
Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His								
	270		275		280		285	
GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC	1212							
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser								
	290		295		300			
TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC	1260							
Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu								
	305		310		315			
TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA	1308							
Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys								
	320		325		330			
TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT	1356							
Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile								

335	340	345	
TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC			1404
Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser			
350	355	360	365
AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG			1452
Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu			
	370	375	380
GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC			1500
Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro			
	385	390	395
TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG			1548
Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu			
	400	405	410
GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC			1596
Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp			
	415	420	425
ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC			1644
Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile			
	430	435	440
ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA			1692
Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val			
	450	455	460
CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA			1740
Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys			
	465	470	475
CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA			1788
Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu			
	480	485	490
CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC			1836
Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala			
	495	500	505
TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT			1884
Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val			
	510	515	520
GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT			1935
Glu Ser Gln Asp Val Lys Ile			
	530		
AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT			1995
AACTTGTTTC TCAGACTCTT TCTTCACTAC GTGTTACACAG GCTGCTAATA TTAAACCTTT			2055
CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTTATTCTT TATATATGGA			2115
CAGCTTTATT TTAAATGTGG TTTTGTATGC CTTTFTTTTAA GTGGGTTTTT ATGAACTGCA			2175
TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTTC			2235
ATAAAACGGT GCTTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA			2295
AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA			2355
GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC			2415
TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTGTA			2475
ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTGTG			2535
CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTAAGTTGCA			2595
AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA			2655
AGAAGTTTAA AGCATCTGTA AATTTGGACT GTTTTCCTTC AACCACCATT TTTTTTGTGG			2715
TTATTATTTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC			2775
ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG			2835
TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTTA			2895
TATTTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC			2932

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Thr	Gln	Leu	Tyr	Ile	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Tyr	Leu	Phe
1				5					10					15	
Ile	Ile	Ser	Arg	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly
			20					25					30		
Thr	Gly	Met	Lys	Ser	Asp	Ser	Asp	Gln	Lys	Lys	Ser	Glu	Asn	Gly	Val
		35					40					45			
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser
	50					55					60				
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly
65					70					75					80
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu
				85					90					95	
Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp
			100						105				110		
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn
		115					120						125		
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly
	130					135						140			
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	Ile	Ser	Met
145					150					155					160
Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr
				165					170					175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	Asn	Arg	Asp
			180					185					190		
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp
		195					200					205			
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu
	210					215						220			
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val
225					230					235					240
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu
				245					250					255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe
			260					265					270		
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile
		275					280					285			
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln
	290					295						300			
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe
305					310					315					320
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr
				325					330					335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr
			340					345					350		
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile
		355					360					365			
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
	370					375					380				
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro	Leu	Asn	Thr
385					390					395					400
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser

Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val		
		115					120					125					
GGC	ATC	ATC	GCC	GGC	CCG	GTG	TTC	CTC	CTG	TTC	CTC	ATC	ATC	ATC	ATT	432	
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile		
		130					135					140					
GTT	TTC	CTT	GTC	ATT	AAC	TAT	CAT	CAG	CGT	GTC	TAT	CAC	AAC	CGC	CAG	480	
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln		
		145				150				155					160		
AGA	CTG	GAC	ATG	GAA	GAT	CCC	TCA	TGT	GAG	ATG	TGT	CTC	TCC	AAA	GAC	528	
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp		
				165					170						175		
AAG	ACG	CTC	CAG	GAT	CTT	GTC	TAC	GAT	CTC	TCC	ACC	TCA	GGG	TCT	GGC	576	
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly		
				180					185					190			
TCA	GGG	TTA	CCC	CTC	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	ACC	ATC	GTT	624	
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val		
		195					200					205					
TTA	CAA	GAG	ATT	ATT	GGC	AAG	GGT	CGG	TTT	GGG	GAA	GTA	TGG	CGG	GGC	672	
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly		
		210				215					220						
CGC	TGG	AGG	GGT	GGT	GAT	GTG	GCT	GTG	AAA	ATA	TTC	TCT	TCT	CGT	GAA	720	
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu		
					230				235						240		
GAA	CGG	TCT	TGG	TTC	AGG	GAA	GCA	GAG	ATA	TAC	CAG	ACG	GTC	ATG	CTG	768	
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu		
				245					250					255			
CGC	CAT	GAA	AAC	ATC	CTT	GGA	TTT	ATT	GCT	GCT	GAC	AAT	AAA	GAT	AAT	816	
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn		
			260					265					270				
GGC	ACC	TGG	ACA	CAG	CTG	TGG	CTT	GTT	TCT	GAC	TAT	CAT	GAG	CAC	GGG	864	
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly		
		275					280					285					
TCC	CTG	TTT	GAT	TAT	CTG	AAC	CGG	TAC	ACA	GTG	ACA	ATT	GAG	GGG	ATG	912	
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met		
		290				295					300						
ATT	AAG	CTG	GCC	TTG	TCT	GCT	GCT	AGT	GGG	CTG	GCA	CAC	CTG	CAC	ATG	960	
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met		
					310					315					320		
GAG	ATC	GTG	GGC	ACC	CAA	GGG	AAG	CCT	GGA	ATT	GCT	CAT	CGA	GAC	TTA	1008	
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu		
				325					330					335			
AAG	TCA	AAG	AAC	ATT	CTG	GTG	AAG	AAA	AAT	GGC	ATG	TGT	GCC	ATA	GCA	1056	
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala		
			340					345					350				
GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCA	GTC	ACT	GAC	ACC	ATT	GAC	1104	
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp		
		355					360					365					
ATT	GCC	CCG	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	GCC	CCT	GAA	1152	
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu		
		370				375					380						
GTA	CTT	GAT	GAA	ACC	ATT	AAT	ATG	AAA	CAC	TTT	GAC	TCC	TTT	AAA	TGT	1200	
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys		
		385				390				395					400		
GCT	GAT	ATT	TAT	GCC	CTC	GGG	CTT	GTA	TAT	TGG	GAG	ATT	GCT	CGA	AGA	1248	
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg		
				405					410					415			
TGC	AAT	TCT	GGA	GGA	GTC	CAT	GAA	GAA	TAT	CAG	CTG	CCA	TAT	TAC	GAC	1296	

Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	
			420					425					430			
TTA	GTG	CCC	TCT	GAC	CCT	TCC	ATT	GAG	GAA	ATG	CGA	AAG	GTT	GTA	TGT	1344
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	
		435					440					445				
GAT	CAG	AAG	CTG	CGT	CCC	AAC	ATC	CCC	AAC	TGG	TGG	CAG	AGT	TAT	GAG	1392
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu	
		450				455					460					
GCA	CTG	CGG	GTG	ATG	GGG	AAG	ATG	ATG	CGA	GAG	TGT	TGG	TAT	GCC	AAC	1440
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn	
		465				470				475					480	
GGC	GCA	GCC	CGC	CTG	ACG	GCC	CTG	CGC	ATC	AAG	AAG	ACC	CTC	TCC	CAG	1488
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln	
			485						490				495			
CTC	AGC	GTG	CAG	GAA	GAC	GTG	AAG	ATC	TA	ACTGCTCC	CTCTCTCCAC					1535
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile								
			500				505									
ACGGAGCTCC	TGGCAGCGAG	AACTACGCAC	AGCTGCCGCG	TTGAGCGTAC	GATGGAGGCC											1595
TACCTCTCGT	TTCTGCCAG	CCCTCTGTGG	CCAGGAGCCC	TGGCCCGCAA	GAGGGACAGA											1655
GCCCGGGAGA	GACTCGCTCA	CTCCCATGTT	GGGTTTGAGA	CAGACACCTT	TTCTATTTAC											1715
CTCCTAATGG	CATGGAGACT	CTGAGAGCGA	ATTGTGTGGA	GA	ACTCAGTG	CCACACCTCG										1775
AACTGGTTGT	AGTGGGAAGT	CCCGCGAAAC	CCGGTGCATC	TGGCACGTGG	CCAGGAGCCA											1835
TGACAGGGGC	GCTTGGGAGG	GGCCGGAGGA	ACCGAGGTGT	TGCCAGTGCT	AAGCTGCCCT											1895
GAGGGTTTCC	TTCGGGGACC	AGCCACAGC	ACACCAAGGT	GGCCCGGAAG	AACCAGAAGT											1955
GCAGCCCCCTC	TCACAGGCAG	CTCTGAGCCG	CGCTTTCCCC	TCCTCCCTGG	GATGGACGCT											2015
GCCGGGAGAC	TGCCAGTGGA	GACGGAATCT	GCCGCTTTGT	CTGTCCAGCC	GTGTGTGCAT											2075
GTGCCGAGGT	GCGTCCCCCG	TTGTGCCTGG	TTCGTGCCAT	GCCCTTACAC	GTGCGTGTGA											2135
GTGTGTGTGT	GTGTCTGTAG	GTGCGCACTT	ACCTGCTTGA	GCTTTCTGTG	CATGTGCAGG											2195
TCGGGGGTGT	GGTCGTCATG	CTGTCCGTGC	TTGCTGGTGC	CTCTTTTCAG	TAGTGAGCAG											2255
CATCTAGTTT	CCCTGGTGCC	CTTCCCTGGA	GGTCTCTCCC	TCCCCCAGAG	CCCCTCATGC											2315
CACAGTGGTA	CTCTGTGT															2333

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu	
1				5					10					15		
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Val	Gln	Ala	Leu	
		20						25					30			
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Ala	Asn	Tyr	Thr	Cys	Glu	Thr	
		35					40					45				
Asp	Gly	Ala	Cys	Met	Val	Ser	Phe	Phe	Asn	Leu	Asp	Gly	Met	Glu	His	
	50					55					60					
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys	
	65				70					75					80	
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys	
			85						90					95		
Tyr	Thr	Asp	Tyr	Cys	Asn	Arg	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His	
		100						105					110			
Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val	
		115					120					125				
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile	

130	135	140
Val Phe Leu Val Ile Asn Tyr His Gln Arg	Val Tyr His Asn Arg Gln	
145	150	155
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp		160
	165	170
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly		175
	180	185
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val		190
	195	200
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly		205
	210	215
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu		220
225	230	235
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu		240
	245	250
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn		255
	260	265
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly		270
	275	280
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met		285
290	295	300
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met		305
	310	315
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu		320
	325	330
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala		335
	340	345
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp		350
	355	360
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu		365
370	375	380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys		385
	390	395
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg		400
	405	410
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp		415
	420	425
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys		430
	435	440
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu		445
450	455	460
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn		465
	470	475
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln		480
	485	490
Leu Ser Val Gln Glu Asp Val Lys Ile		495
	500	505

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
GGCGAGGCGA GGTTCGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG      60
CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG      109
      Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg
              1              5              10
CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG CTG      157
Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Leu
              15              20              25
CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA      205
Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys
              30              35              40
GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA      253
Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr
              45              50              55
GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT      301
Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile
              60              65              70              75
GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA      349
Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys
              80              85              90
ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT      397
Thr Gly Ser Val Thr Thr Thr Tyr Cys Asn Gln Asp His Cys Asn
              95              100              105
AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT      445
Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro
              110              115              120
GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC      493
Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile
              125              130              135
TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC      541
Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His
              140              145              150              155
CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT      589
His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile
              160              165              170
TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA      637
Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser
              175              180              185
GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA      685
Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg
              190              195              200
ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT      733
Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val
              205              210              215
TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC      781
Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser
              220              225              230              235
TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT      829
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr
              240              245              250
GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT      877
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Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
255 260 265	
AAA GAC AAT GGT ACT TGG ACT CAG CTC TGG TTG GTG TCA GAT TAT CAT	925
Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
270 275 280	
GAG CAT GGA TCC CTT TTT GAT TAC TTA AAC AGA TAC ACA GTT ACT GTG	973
Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val	
285 290 295	
GAA GGA ATG ATA AAA CTT GCT CTG TCC ACG GCG AGC GGT CTT GCC CAT	1021
Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His	
300 305 310 315	
CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAG CCA GCC ATT GCT CAT	1069
Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His	
320 325 330	
AGA GAT TTG AAA TCA AAG AAT ATC TTG GTA AAG AAG AAT GGA ACT TGC	1117
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys	
335 340 345	
TGT ATT GCA GAC TTA GGA CTG GCA GTA AGA CAT GAT TCA GCC ACA GAT	1165
Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp	
350 355 360	
ACC ATT GAT ATT GCT CCA AAC CAC AGA GTG GGA ACA AAA AGG TAC ATG	1213
Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met	
365 370 375	
GCC CCT GAA GTT CTC GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA TCC	1261
Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser	
380 385 390 395	
TTC AAA CGT GCT GAC ATC TAT GCA ATG GGC TTA GTA TTC TGG GAA ATT	1309
Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile	
400 405 410	
GCT CGA CGA TGT TCC ATT GGT GGA ATT CAT GAA GAT TAC CAA CTG CCT	1357
Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA	1405
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys	
430 435 440	
GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG	1453
Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln	
445 450 455	
AGC TGT GAA GCC TTG AGA GTA ATG GCT AAA ATT ATG AGA GAA TGT TGG	1501
Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp	
460 465 470 475	
TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA	1549
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA	1595
Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met	
495 500	
GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT TTGGGAGGTC	1655
AGTTGTTCTA ACTCACTGAG AGGGAACAGA AGGATATTGC TTCCTTTTGC AGCAGTGTA	1715
TAAAGTCAAT TAAAACTTC CCAGGATTTT TTTGGACCCA GGAAACAGCC ATGTGGGTCC	1775
TTTCTGTGCA CTATGAACGC TTCTTTCCCA GGACAGAAAA TGTGTAGTCT ACCTTTATTT	1835
TTTATTAACA AAACCTGTTT TTTAAAAAGA TGATTGCTGG TCTTAACCTT AGGTAACCT	1895
GCTGTGCTGG AGATCATCTT TAAGGGCAAA GGAGTTGGAT TGCTGAATTA CAATGAAACA	1955
TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA GGATTCTGAA	2015
CCACTAGAGT TTCCTTGATT CAGACTTTGA ATGTACTGTT CTATAGTTTT TCAGGATCTT	2075
AAAATAACA CTTATAAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA TAGTAGTGAG	2135
GAACATAATT CATGCAATTG TATTTTGTAT ACTATTATTG TTCTTTCAC TATTCAGAAC	2195

ATTACATGCC TTCAAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT GTGTCTTTCT 2255
 AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT 2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Glu	Ala	Ala	Val	Ala	Ala	Pro	Arg	Pro	Arg	Leu	Leu	Leu	Leu	Val
1				5					10					15	
Leu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Pro	Gly	Ala	Thr
			20					25					30		
Ala	Leu	Gln	Cys	Phe	Cys	His	Leu	Cys	Thr	Lys	Asp	Asn	Phe	Thr	Cys
		35					40					45			
Val	Thr	Asp	Gly	Leu	Cys	Phe	Val	Ser	Val	Thr	Glu	Thr	Thr	Asp	Lys
	50					55					60				
Val	Ile	His	Asn	Ser	Met	Cys	Ile	Ala	Glu	Ile	Asp	Leu	Ile	Pro	Arg
65				70					75					80	
Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	Thr	Gly	Ser	Val	Thr
			85					90						95	
Thr	Thr	Tyr	Cys	Cys	Asn	Gln	Asp	His	Cys	Asn	Lys	Ile	Glu	Leu	Pro
		100					105						110		
Thr	Thr	Val	Lys	Ser	Ser	Pro	Gly	Leu	Gly	Pro	Val	Glu	Leu	Ala	Ala
	115					120						125			
Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	Ile	Ser	Leu	Met	Leu	Met
130					135					140					
Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	His	His	Arg	Val	Pro	Asn
145				150					155					160	
Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	Ser	Glu	Gly	Thr	Thr
			165					170					175		
Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	Gly	Ser	Gly	Ser	Gly
		180					185					190			
Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	Thr	Ile	Val	Leu	Gln
	195					200						205			
Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	Lys	Trp
210				215						220					
Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	Glu	Arg
225				230					235					240	
Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	Arg	His
			245					250					255		
Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	Gly	Thr
	260						265						270		
Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	Ser	Leu
	275					280						285			
Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	Glu	Gly	Met	Ile	Lys
290				295						300					
Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	Glu	Ile
305				310					315					320	
Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser
			325					330					335		
Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu
	340						345					350			
Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	Thr	Ile	Asp	Ile	Ala
	355					360						365			

Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu
 370 375 380
 Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp
 385 390 395 400
 Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser
 405 410 415
 Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val
 420 425 430
 Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln
 435 440 445
 Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu
 450 455 460
 Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
 465 470 475 480
 Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
 485 490 495
 Gln Gln Glu Gly Ile Lys Met
 500

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG CCCTTCCAG TCCCCGGAGC CGCCGCGCCA CGCGCGCATG ATCAAGACCT	60
TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC	120
GGGGGTGCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC CTGTTGCCGG	180
CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC	240
ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC	288
Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala	
1 5 10 15	
TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC	336
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn	
20 25 30	
TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA	384
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser	
35 40 45	
TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC	432
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val	
50 55 60	
TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC	480
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro	
65 70 75 80	
ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC	528
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His	

85										90					95					
AAC	GTG	TCT	CTG	ATG	CTG	GAG	GCC	ACC	CAA	ACT	CCT	TCG	GAG	GAG	CCA	576				
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro					
100										105					110					
GAA	GTT	GAT	GCC	CAT	CTG	CCT	CTG	ATC	CTG	GGT	CCT	GTG	CTG	GCC	TTG	624				
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu					
115										120					125					
CCG	GTC	CTG	GTG	GCC	CTG	GGT	GCT	CTG	GGC	TTG	TGG	CGT	GTC	CGG	CGG	672				
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg					
130										135					140					
AGG	CAG	GAG	AAG	CAG	CGG	GAT	TTG	CAC	AGT	GAC	CTG	GGC	GAG	TCC	AGT	720				
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser					
145										150					155					
CTC	ATC	CTG	AAG	GCA	TCT	GAA	CAG	GCA	GAC	AGC	ATG	TTG	GGG	GAC	TTC	768				
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe					
165										170					175					
CTG	GAC	AGC	GAC	TGT	ACC	ACG	GGC	AGC	GGC	TCG	GGG	CTC	CCC	TTC	TTG	816				
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu					
180										185					190					
GTG	CAG	AGG	ACG	GTA	GCT	CGG	CAG	GTT	GCG	CTG	GTA	GAG	TGT	GTG	GGA	864				
Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly					
195										200					205					
AAG	GGC	CGA	TAT	GGC	GAG	GTG	TGG	CGC	GGT	TCG	TGG	CAT	GGC	GAA	AGC	912				
Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	His	Gly	Glu	Ser					
210										215					220					
GTG	GCG	GTC	AAG	ATT	TTC	TCC	TCA	CGA	GAT	GAG	CAG	TCC	TGG	TTC	CGG	960				
Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg					
225										230					235					
GAG	ACG	GAG	ATC	TAC	AAC	ACA	GTT	CTG	CTT	AGA	CAC	GAC	AAC	ATC	CTA	1008				
Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu					
245										250					255					
GGC	TTC	ATC	GCC	TCC	GAC	ATG	ACT	TCG	CGG	AAC	TCG	AGC	ACG	CAG	CTG	1056				
Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu					
260										265					270					
TGG	CTC	ATC	ACC	CAC	TAC	CAT	GAA	CAC	GGC	TCC	CTC	TAT	GAC	TTT	CTG	1104				
Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu					
275										280					285					
CAG	AGG	CAG	ACG	CTG	GAG	CCC	CAG	TTG	GCC	CTG	AGG	CTA	GCT	GTG	TCC	1152				
Gln	Arg	Gln	Thr	Leu	Glu	Pro	Gln	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser					
290										295					300					
CCG	GCC	TGC	GGC	CTG	GCG	CAC	CTA	CAT	GTG	GAG	ATC	TTT	GGC	ACT	CAA	1200				
Pro	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln					
305										310					315					
GGC	AAA	CCA	GCC	ATT	GCC	CAT	CGT	GAC	CTC	AAG	AGT	CGC	AAT	GTG	CTG	1248				
Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Leu					
325										330					335					
GTC	AAG	AGT	AAC	TTG	CAG	TGT	TGC	ATT	GCA	GAC	CTG	GGA	CTG	GCT	GTG	1296				
Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val					
340										345					350					
ATG	CAC	TCA	CAA	AGC	AAC	GAG	TAC	CTG	GAT	ATC	GGC	AAC	ACA	CCC	CGA	1344				
Met	His	Ser	Gln	Ser	Asn	Glu	Tyr	Leu	Asp	Ile	Gly	Asn	Thr	Pro	Arg					
355										360					365					
GTG	GGT	ACC	AAA	AGA	TAC	ATG	GCA	CCC	GAG	GTG	CTG	GAT	GAG	CAC	ATC	1392				
Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	His	Ile					
370										375					380					
CGC	ACA	GAC	TGC	TTT	GAG	TCG	TAC	AAG	TGG	ACA	GAC	ATC	TGG	GCC	TTT	1440				
Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	Phe					

385		390		395		400	
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT							1488
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile							
	405		410		415		
GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC							1536
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro							
	420		425		430		
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC							1584
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro							
	435		440		445		
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC							1632
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala							
	450		455		460		
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC							1680
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr							
	465		470		475		480
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG							1728
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu							
	485		490		495		
AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCAGGCT TCCTCTGCCT							1776
Lys Pro Lys Val Ile His							
	500						
AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGGTA GAGGGAGTGA AGAGAGTGTG							1836
CACGCTGCCC TGTGTGTGCC TGCTCAGCTT GCTCCAGCC CATCCAGCCA AAAATACAGC							1896
TGAGCTGAAA TTCAAAAAA AAAAAA							1922

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Thr	Leu	Gly	Ser	Phe	Arg	Arg	Gly	Leu	Leu	Met	Leu	Ser	Val	Ala
1				5					10					15	
Leu	Gly	Leu	Thr	Gln	Gly	Arg	Leu	Ala	Lys	Pro	Ser	Lys	Leu	Val	Asn
		20						25					30		
Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Arg	Pro	Phe	Cys	Gln	Gly	Ser
		35					40					45			
Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Gln	Gly	Arg	His	Pro	Gln	Val
	50					55				60					
Tyr	Arg	Gly	Cys	Gly	Ser	Leu	Asn	Gln	Glu	Leu	Cys	Leu	Gly	Arg	Pro
	65				70				75					80	
Thr	Glu	Phe	Leu	Asn	His	His	Cys	Cys	Tyr	Arg	Ser	Phe	Cys	Asn	His
			85						90					95	
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro
		100						105					110		
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu
	115						120					125			
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg
	130					135					140				
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser
	145				150				155					160	
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe
			165					170						175	
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu

(B) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATTTCATGAGA	TGGAAGCATA	GGTCAAAGCT	GTTCGGAGAA	ATTGGAACATA	CAGTTTTATC	60
TAGCCACATC	TCTGAGAATT	CTGAAGAAAG	CAGCAGGTGA	AAGTCATTGC	CAAGTGATTT	120
TGTTCTGTAA	GGAAGCCTCC	CTCATTCACT	TACACCAGTG	AGACAGCAGG	ACCAGTCATT	180
CAAAGGGCCG	TGTACAGGAC	GCGTGGCAAT	CAGACA	ATG	ACT CAG CTA TAC ACT	234
			Met	Thr	Gln Leu Tyr Thr	
			1		5	
TAC	ATC	AGA	TTA	CTG	GGA GCC TGT CTG TTC ATC ATT TCT CAT GTT CAA	282
Tyr	Ile	Arg	Leu	Leu	Gly Ala Cys Leu Phe Ile Ile Ser His Val Gln	
		10			15	20
GGG	CAG	AAT	CTA	GAT	AGT ATG CTC CAT GGC ACT GGT ATG AAA TCA GAC	330
Gly	Gln	Asn	Leu	Asp	Ser Met Leu His Gly Thr Gly Met Lys Ser Asp	
		25			30	35
TTG	GAC	CAG	AAG	AAG	CCA GAA AAT GGA GTG ACT TTA GCA CCA GAG GAT	378
Leu	Asp	Gln	Lys	Lys	Pro Glu Asn Gly Val Thr Leu Ala Pro Glu Asp	
		40			45	50
ACC	TTG	CCT	TTC	TTA	AAG TGC TAT TGC TCA GGA CAC TGC CCA GAT GAT	426
Thr	Leu	Pro	Phe	Leu	Lys Cys Tyr Cys Ser Gly His Cys Pro Asp Asp	
		55			60	65
GCT	ATT	AAT	AAC	ACA	TGC ATA ACT AAT GGC CAT TGC TTT GCC ATT ATA	474
Ala	Ile	Asn	Asn	Thr	Cys Ile Thr Asn Gly His Cys Phe Ala Ile Ile	
			75		80	85
GAA	GAA	GAT	GAT	CAG	GGA GAA ACC ACA TTA ACT TCT GGG TGT ATG AAG	522
Glu	Glu	Asp	Asp	Gln	Gly Glu Thr Thr Leu Thr Ser Gly Cys Met Lys	
		90			95	100
TAT	GAA	GGC	TCT	GAT	TTT CAA TGC AAG GAT TCA CCG AAA GCC CAG CTA	570
Tyr	Glu	Gly	Ser	Asp	Phe Gln Cys Lys Asp Ser Pro Lys Ala Gln Leu	
		105			110	115
CGC	AGG	ACA	ATA	GAA	TGT TGT CGG ACC AAT TTG TGC AAC CAG TAT TTG	618
Arg	Arg	Thr	Ile	Glu	Cys Cys Arg Thr Asn Leu Cys Asn Gln Tyr Leu	
		120			125	130
CAG	CCT	ACA	CTG	CCC	CCT GTT GTT ATA GGT CCG TTC TTT GAT GGC AGC	666
Gln	Pro	Thr	Leu	Pro	Pro Val Val Ile Gly Pro Phe Phe Asp Gly Ser	
			135		140	145
ATC	CGA	TGG	CTG	GTT	GTG CTC ATT TCC ATG GCT GTC TGT ATA GTT GCT	714
Ile	Arg	Trp	Leu	Val	Val Leu Ile Ser Met Ala Val Cys Ile Val Ala	
			155		160	165
ATG	ATC	ATC	TTC	TCC	AGC TGC TTT TGC TAT AAG CAT TAT TGT AAG AGT	762
Met	Ile	Ile	Phe	Ser	Ser Cys Phe Cys Tyr Lys His Tyr Cys Lys Ser	
			170		175	180
ATC	TCA	AGC	AGG	GGT	CGT TAC AAC CGT GAT TTG GAA CAG GAT GAA GCA	810
Ile	Ser	Ser	Arg	Gly	Arg Tyr Asn Arg Asp Leu Glu Gln Asp Glu Ala	
			185		190	195
TTT	ATT	CCA	GTA	GGA	GAA TCA TTG AAA GAC CTG ATT GAC CAG TCC CAA	858
Phe	Ile	Pro	Val	Gly	Glu Ser Leu Lys Asp Leu Ile Asp Gln Ser Gln	
		200			205	210
AGC	TCT	GGG	AGT	GGA	TCT GGA TTG CCT TTA TTG GTT CAG CGA ACT ATT	906
Ser	Ser	Gly	Ser	Gly	Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile	
			215		220	225
GCC	AAA	CAG	ATT	CAG	ATG GTT CGG CAG GTT GGT AAA GGC CGC TAT GGA	954
Ala	Lys	Gln	Ile	Gln	Met Val Arg Gln Val Gly Lys Gly Arg Tyr Gly	
			235		240	245
GAA	GTA	TGG	ATG	GGT	AAA TGG CGT GGT GAA AAA GTG GCT GTC AAA GTG	1002
Glu	Val	Trp	Met	Gly	Lys Trp Arg Gly Glu Lys Val Ala Val Lys Val	
			250		255	260
TTT	TTT	ACC	ACT	GAA	GAA GCT AGC TGG TTT AGA GAA ACA GAA ATC TAC	1050

Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	
		265					270					275				
CAG	ACG	GTG	TTA	ATG	CGT	CAT	GAA	AAT	ATA	CTT	GGT	TTT	ATA	GCT	GCA	1098
Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	
		280					285				290					
GAC	ATT	AAA	GGC	ACT	GGT	TCC	TGG	ACT	CAG	CTG	TAT	TTG	ATT	ACT	GAT	1146
Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	
		295			300				305					310		
TAC	CAT	GAA	AAT	GGA	TCT	CTC	TAT	GAC	TTC	CTG	AAA	TGT	GCC	ACA	CTA	1194
Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu	
			315						320					325		
GAC	ACC	AGA	GCC	CTA	CTC	AAG	TTA	GCT	TAT	TCT	GCT	GCT	TGT	GGT	CTG	1242
Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu	
		330						335					340			
TGC	CAC	CTC	CAC	ACA	GAA	ATT	TAT	GGT	ACC	CAA	GGG	AAG	CCT	GCA	ATT	1290
Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	
		345					350				355					
GCT	CAT	CGA	GAC	CTG	AAG	AGC	AAA	AAC	ATC	CTT	ATT	AAG	AAA	AAT	GGA	1338
Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly	
		360				365				370						
AGT	TGC	TGT	ATT	GCT	GAC	CTG	GGC	CTA	GCT	GTT	AAA	TTC	AAC	AGT	GAT	1386
Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp	
					380				385					390		
ACA	AAT	GAA	GTT	GAC	ATA	CCC	TTG	AAT	ACC	AGG	GTG	GGC	ACC	AAG	CGG	1434
Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	
				395					400					405		
TAC	ATG	GCT	CCA	GAA	GTG	CTG	GAT	GAA	AGC	CTG	AAT	AAA	AAC	CAT	TTC	1482
Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe	
		410						415					420			
CAG	CCC	TAC	ATC	ATG	GCT	GAC	ATC	TAT	AGC	TTT	GGT	TTG	ATC	ATT	TGG	1530
Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp	
		425					430					435				
GAA	ATG	GCT	CGT	CGT	TGT	ATT	ACA	GGA	GGA	ATC	GTG	GAG	GAA	TAT	CAA	1578
Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	
		440				445					450					
TTA	CCA	TAT	TAC	AAC	ATG	GTG	CCC	AGT	GAC	CCA	TCC	TAT	GAG	GAC	ATG	1626
Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	
					460				465					470		
CGT	GAG	GTT	GTG	TGT	GTG	AAA	CGC	TTG	CGG	CCA	ATC	GTG	TCT	AAC	CGC	1674
Arg	Glu	Val	Val	Cys	Val	Lys	Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg	
				475					480					485		
TGG	AAC	AGC	GAT	GAA	TGT	CTT	CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	1722
Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu	
		490						495					500			
TGT	TGG	GCC	CAT	AAT	CCA	GCC	TCC	AGA	CTC	ACA	GCT	TTG	AGA	ATC	AAG	1770
Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	
		505					510						515			
AAG	ACA	CTT	GCA	AAA	ATG	GTT	GAA	TCC	CAG	GAT	GTA	AAG	ATT			1812
Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln	Asp	Val	Lys	Ile			
		520				525					530					
TGACAATTAA	ACAATTTTGA	GGGAGAATTT	AGACTGCAAG	AACTTCTTCA	CCCAAGGAAT											1872
GGGTGGGATT	AGCATGGAAT	AGGATGTTGA	CTTGGTTTCC	AGACTCCTTC	CTCTACATCT											1932
TCACAGGCTG	CTAACAGTAA	ACCTTACCGT	ACTCTACAGA	ATACAAGATT	GGAAGTTGGA											1992
ACTTCAAACA	TGTCATTCTT	TATATATGAC	AGCTTTGTTT	TAATGTGGGG	TTTTTTTGTT											2052
TGCTTTTTTTT	GTTTTGTT															2070

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Thr	Gln	Leu	Tyr	Thr	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Cys	Leu	Phe
1				5					10					15	
Ile	Ile	Ser	His	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly
			20					25					30		
Thr	Gly	Met	Lys	Ser	Asp	Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val
		35					40					45			
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser
	50					55					60				
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly
65					70				75					80	
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu
				85					90					95	
Thr	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp
		100						105					110		
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn
	115					120						125			
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly
	130					135				140					
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met
145					150				155					160	
Ala	Val	Cys	Ile	Val	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr
				165					170					175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp
		180						185					190		
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp
	195					200					205				
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu
	210					215				220					
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val
225				230					235					240	
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu
				245					250					255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe
		260						265					270		
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile
	275					280						285			
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln
	290					295				300					
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe
305					310					315				320	
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr
				325					330					335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr
		340						345					350		
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile
	355						360					365			
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
	370					375					380				
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr
385					390					395				400	

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
405 410 415
Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
420 425 430
Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
435 440 445
Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
450 455 460
Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
465 470 475 480
Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
485 490 495
Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
500 505 510
Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
515 520 525
Asp Val Lys Ile
530

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mouse
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu	
1 5 10	
GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC	96
Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile	
15 20 25	
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC	144
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr	
30 35 40 45	
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC	192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly	
50 55 60	
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT	240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro	
65 70 75	
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA	288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr	
80 85 90	
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC	336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro	
95 100 105	

AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG	384
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val	
110 115 120 125	
GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC	432
Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile	
130 135 140	
ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT	480
Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His	
145 150 155	
AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC	528
Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu	
160 165 170	
TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA	576
Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser	
175 180 185	
GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA	624
Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg	
190 195 200 205	
ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA	672
Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val	
210 215 220	
TGG CGT GGT CGC TGG AGG GGT GGT GAC GTG GCT GTG AAA ATC TTC TCT	720
Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser	
225 230 235	
TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC	768
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr	
240 245 250	
GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT	816
Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
255 260 265	
AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC	864
Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
270 275 280 285	
GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT	912
Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile	
290 295 300	
GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC	960
Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His	
305 310 315	
CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT	1008
Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His	
320 325 330	
CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT	1056
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys	
335 340 345	
GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC	1104
Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp	
350 355 360 365	
ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG	1152
Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met	
370 375 380	
GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC	1200
Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser	
385 390 395	
TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT	1248
Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile	
400 405 410	

GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG	1296
Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG	1344
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys	
430 435 440 445	
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG	1392
Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln	
450 455 460	
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG	1440
Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp	
465 470 475	
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT	1488
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC	1534
Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile	
495 500 505	
CTCTGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT	1594
GGAGGCCTAT CCTCTTGTTT CTGCCCCGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA	1654
CAGAGCCTGG GAGACGCGCG CACTCCCGTT GGGTTTGAGA CAGACACTTT TTATATTTAC	1714
CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACTCAAAC	1774
GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG	1834
CTCGCCAGGA GCGGCCCCCA TACCTTGTGG TCCACTGGGC TGCAGGTTTT CCTCCAGGGA	1894
CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCAGGAAGT TTCTCCCTCC TTCCCGTAGC	1954
AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCCCTA GAGACACAAC	2014
CTGCTGCCTG TCTGTCCAGC CAAGTGCAGC TGTGCCGAGG TGTGTCCCAC ATTGTGCCTG	2074
GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACACTTA	2134
ACCTGCTTGA GCTTCTGTGC ATGTGT	2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu
1				5					10					15	
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Ile	Gln	Ala	Leu
			20					25					30		
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Thr	Asn	Tyr	Thr	Cys	Glu	Thr
			35				40					45			
Asp	Gly	Ala	Cys	Met	Val	Ser	Ile	Phe	Asn	Leu	Asp	Gly	Val	Glu	His
	50					55					60				
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys
	65				70					75				80	
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys
			85					90					95		
Tyr	Ile	Asp	Phe	Cys	Asn	Lys	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His
			100					105					110		
Leu	Lys	Glu	Pro	Ala	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val
			115					120				125			
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile
	130					135					140				
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln

145		150		155		160
Arg	Leu	Asp	Met	Glu	Asp	Pro
		165		170		175
Lys	Thr	Leu	Gln	Asp	Leu	Val
		180		185		190
Ser	Gly	Leu	Pro	Leu	Phe	Val
		195		200		205
Leu	Gln	Glu	Ile	Ile	Gly	Lys
		210		215		220
Arg	Trp	Arg	Gly	Gly	Asp	Val
		225		230		235
Glu	Arg	Ser	Trp	Phe	Arg	Glu
		245		250		255
Arg	His	Glu	Asn	Ile	Leu	Gly
		260		265		270
Gly	Thr	Trp	Thr	Gln	Leu	Trp
		275		280		285
Ser	Leu	Phe	Asp	Tyr	Leu	Asn
		290		295		300
Ile	Lys	Leu	Ala	Leu	Ser	Ala
		305		310		315
Glu	Ile	Val	Gly	Thr	Gln	Gly
		325		330		335
Lys	Ser	Lys	Asn	Ile	Leu	Val
		340		345		350
Asp	Leu	Gly	Leu	Ala	Val	Arg
		355		360		365
Ile	Ala	Pro	Asn	Gln	Arg	Val
		370		375		380
Val	Leu	Asp	Glu	Thr	Ile	Asn
		385		390		395
Ala	Asp	Ile	Tyr	Ala	Leu	Gly
		405		410		415
Cys	Asn	Ser	Gly	Gly	Val	His
		420		425		430
Leu	Val	Pro	Ser	Asp	Pro	Ser
		435		440		445
Asp	Gln	Lys	Leu	Arg	Pro	Asn
		450		455		460
Ala	Leu	Arg	Val	Met	Gly	Lys
		465		470		475
Gly	Ala	Ala	Arg	Leu	Thr	Ala
		485		490		495
Leu	Ser	Val	Gln	Glu	Asp	Val
		500		505		

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1952 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```
AAGCGGCGGC AGAAGTTGCC GCGTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGACC      60
TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC      120
AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT      180
GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG      228
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys
    1           5           10
AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA      276
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu
    15          20          25          30
CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC      324
Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile
    35          40          45
TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT      372
Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser
    50          55          60
GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT      420
Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp
    65          70          75
TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA      468
Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu
    80          85          90
TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG      516
Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu
    95          100         105         110
CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG      564
Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys
    115         120         125
GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT      612
Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile
    130         135         140
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG      660
Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg
    145         150         155
TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG      708
Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu
    160         165         170
TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA      756
Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser
    175         180         185         190
GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG      804
Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met
    195         200         205
GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG      852
Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys
    210         215         220
TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA      900
Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu
    225         230         235
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG      948
Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg
    240         245         250
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CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG	996
His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly	
255 260 265 270	
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC	1044
Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser	
275 280 285	
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG	1092
Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu	
290 295 300	
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA	1140
Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu	
305 310 315	
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA	1188
Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys	
320 325 330	
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC	1236
Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp	
335 340 345 350	
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC	1284
Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile	
355 360 365	
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG	1332
Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val	
370 375 380	
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT	1380
Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	
385 390 395	
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT	1428
Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys	
400 405 410	
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG	1476
Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu	
415 420 425 430	
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG	1524
Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met	
435 440 445	
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT	1572
Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys	
450 455 460	
CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT	1620
Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro	
465 470 475	
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG	1668
Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met	
480 485 490	
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA	1722
Ser Glu Ser Gln Asp Ile Lys Leu	
495 500	
ATTTACACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA	1782
GACTTTCTCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT	1842
CATGGCTTTC TGAGGAGGAG AAAGTGTGTTG GGTAAGTTGT TCAAGATATG ATGCATGTTG	1902
CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTTT ATAAAAAAA	1952

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Leu	Leu	Arg	Ser	Ser	Gly	Lys	Leu	Asn	Val	Gly	Thr	Lys	Lys	Glu
1				5				10						15	
Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Pro	Arg	Pro	Lys	Ile	Leu	Arg	Cys
			20					25					30		
Lys	Cys	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	Cys	Ser	
		35				40					45				
Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Ser	Gly	Met	
	50					55					60				
Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln
65					70				75						80
Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	Cys	Cys
			85					90						95	
Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	Pro	Pro
			100					105					110		
Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	Ala	Leu
		115					120					125			
Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	Ile	Leu
	130					135					140				
Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	Tyr	Ser
145					150				155						160
Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	Ser	Leu
			165					170						175	
Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu
		180						185					190		
Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Lys
	195					200						205			
Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg
	210					215					220				
Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser
225					230				235						240
Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu
			245					250						255	
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp
		260						265					270		
Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr
	275					280						285			
Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	Lys	Leu
	290					295					300				
Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Phe
305					310					315					320
Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys
			325					330						335	
Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	Gly
		340						345					350		
Leu	Ala	Val	Lys	Phe	Ile	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Pro
	355					360						365			
Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Pro	Pro	Glu	Val	Leu	Asp
	370					375						380			
Glu	Ser	Leu	Asn	Arg	Asn	His	Phe	Gln	Ser	Tyr	Ile	Met	Ala	Asp	Met
385				390						395					400
Tyr	Ser	Phe	Gly	Leu	Ile	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Cys	Val	Ser
			405					410						415	
Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	His	Asp	Leu	Val	Pro

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
CGGAATTCTG GTGCCATATA 20

(2) INFORMATION FOR SEQ ID NO: 23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
ATTCAAGGGC ACATCAACTT CATTTGTGTC ACTGTTG 37

(2) INFORMATION FOR SEQ ID NO: 24:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
GCGGATCCAC CATGGCGGAG TCGGCC 26

(2) INFORMATION FOR SEQ ID NO: 25:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
AACACCGGGC CGGCGATGAT 20

(2) INFORMATION FOR SEQ ID NO: 26:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
Gly Xaa Gly Xaa Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn

1 5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn

1 5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met

1 5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
5 10 15
Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
20 25 30
Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
35 40 45
Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
50 55 60
Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
65 70 75 80
Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
85 90 95
Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
100 105 110
Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn

Pro	Val	Thr	Pro	Lys	Pro	Pro	Tyr	Tyr	Asn	Ile	Leu	Leu	Tyr	Ser	Leu
130							135				140				
Val	Pro	Leu	Met	Leu	Ile	Ala	Gly	Ile	Val	Ile	Cys	Ala	Phe	Trp	Val
145					150					155					160
Tyr	Arg	His	His	Lys	Met	Ala	Tyr	Pro	Pro	Val	Leu	Val	Pro	Thr	Gln
				165					170					175	
Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Leu	Gly	Leu	Lys	Pro	Leu
			180					185					190		
Gln	Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys
	195						200					205			
Ala	Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln
	210					215					220				
Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly
225					230					235					240
Met	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly
				245				250						255	
Thr	Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys
			260					265					270		
Gly	Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu
	275						280					285			
Leu	Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His
	290					295					300				
Glu	Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His
305					310					315					320
Arg	Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	Leu	Thr	Ala
				325				330						335	
Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Gly	Lys	Ser
		340						345					350		
Ala	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro
	355						360					365			
Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe	Gln	Arg	Asp	Ala	Phe	Leu	Arg
	370					375					380				
Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val	Leu	Trp	Glu	Leu	Ala	Ser	Arg
385					390					395					400
Cys	Thr	Ala	Ala	Asp	Gly	Pro	Val	Asp	Glu	Tyr	Met	Leu	Pro	Phe	Glu
				405				410						415	
Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu	Glu	Asp	Met	Gln	Glu	Val	Val
			420					425				430			
Val	His	Lys	Lys	Lys	Arg	Pro	Val	Leu	Arg	Asp	Tyr	Trp	Gln	Lys	His
		435					440					445			
Ala	Gly	Met	Ala	Met	Leu	Cys	Glu	Thr	Ile	Glu	Glu	Cys	Trp	Asp	His
	450					455					460				
Asp	Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly	Cys	Val	Gly	Glu	Arg	Ile	Thr
465					470					475					480
Gln	Met	Gln	Arg	Leu	Thr	Asn	Ile	Ile	Thr	Thr	Glu	Asp	Ile	Val	Thr
				485				490						495	
Val	Val	Thr	Met	Val	Thr	Asn	Val	Asp	Phe	Pro	Pro	Lys	Glu	Ser	Ser
			500					505					510		
Leu															

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met	Thr	Ala	Pro	Trp	Ala	Ala	Leu	Ala	Leu	Leu	Trp	Gly	Ser	Leu	Cys
			5					10						15	
Ala	Gly	Ser	Gly	Arg	Gly	Glu	Ala	Glu	Thr	Arg	Glu	Cys	Ile	Tyr	Tyr
		20				25						30			
Asn	Ala	Asn	Trp	Glu	Leu	Glu	Arg	Thr	Asn	Gln	Ser	Gly	Leu	Glu	Arg
		35				40						45			
Cys	Glu	Gly	Glu	Gln	Asp	Lys	Arg	Leu	His	Cys	Tyr	Ala	Ser	Trp	Arg
	50				55					60					
Asn	Ser	Ser	Gly	Thr	Ile	Glu	Leu	Val	Lys	Lys	Gly	Cys	Trp	Leu	Asp
65				70					75					80	
Asp	Phe	Asn	Cys	Tyr	Asp	Arg	Gln	Glu	Cys	Val	Ala	Thr	Glu	Glu	Asn
			85					90						95	
Pro	Gln	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Phe	Cys	Asn	Glu	Arg
		100						105					110		
Phe	Thr	His	Leu	Pro	Glu	Pro	Gly	Gly	Pro	Glu	Val	Thr	Tyr	Glu	Pro
		115					120						125		
Pro	Pro	Thr	Ala	Pro	Thr	Leu	Leu	Thr	Val	Leu	Ala	Tyr	Ser	Leu	Leu
		130				135					140				
Pro	Ile	Gly	Gly	Leu	Ser	Leu	Ile	Val	Leu	Leu	Ala	Phe	Trp	Met	Tyr
145				150					155					160	
Arg	His	Arg	Lys	Pro	Pro	Tyr	Gly	His	Val	Asp	Ile	His	Glu	Val	Arg
			165					170						175	
Gln	Cys	Gln	Arg	Trp	Ala	Gly	Arg	Arg	Asp	Gly	Cys	Ala	Asp	Ser	Phe
		180					185						190		
Lys	Pro	Leu	Pro	Phe	Gln	Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu
		195				200						205			
Val	Gly	Leu	Lys	Pro	Leu	Gln	Leu	Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg
	210				215						220				
Phe	Gly	Cys	Val	Trp	Lys	Ala	Gln	Leu	Met	Asn	Asp	Phe	Val	Ala	Val
225				230						235				240	
Lys	Ile	Phe	Pro	Leu	Gln	Asp	Lys	Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu
			245					250						255	
Ile	Phe	Ser	Thr	Pro	Gly	Met	Lys	His	Glu	Asn	Leu	Leu	Gln	Phe	Ile
		260					265						270		
Ala	Ala	Glu	Lys	Arg	Gly	Ser	Asn	Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile
		275					280						285		
Thr	Ala	Phe	His	Asp	Lys	Gly	Ser	Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn
	290				295						300				
Ile	Ile	Thr	Trp	Asn	Glu	Leu	Cys	His	Val	Ala	Glu	Thr	Met	Ser	Arg
305				310						315				320	
Gly	Leu	Ser	Tyr	Leu	His	Glu	Asp	Val	Pro	Trp	Cys	Arg	Gly	Glu	Gly
			325					330						335	
His	Lys	Pro	Ser	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Lys	Asn	Val	Leu
		340					345						350		
Leu	Lys	Ser	Asp	Leu	Thr	Ala	Val	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Val
		355				360						365			
Arg	Phe	Glu	Pro	Gly	Lys	Pro	Pro	Gly	Asp	Thr	His	Gly	Gln	Val	Gly
	370				375							380			
Thr	Arg	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe
385				390						395				400	
Gln	Arg	Asp	Ala	Phe	Leu	Arg	Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val
			405					410					415		
Leu	Trp	Glu	Leu	Val	Ser	Arg	Cys	Lys	Ala	Ala	Asp	Gly	Pro	Val	Asp
		420					425					430			
Glu	Tyr	Met	Leu	Pro	Phe	Glu	Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu

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275	280	285
Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile		
290	295	300
Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln		
305	310	315
Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr		
325	330	335
Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser		
340	345	350
Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys		
355	360	365
Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn		
370	375	380
Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu		
385	390	395
Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser		
405	410	415
Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser		
420	425	430
Arg Met Asn Leu Glu Asn Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr		
435	440	445
Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val		
450	455	460
Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu		
465	470	475
His Pro Cys Val Glu Ser Met Lys Asp Asn Val Leu Arg Asp Arg Gly		
485	490	495
Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn His Gln Gly Ile Gln Met		
500	505	510
Val Cys Glu Thr Leu Thr Glu Cys Trp Asp His Asp Pro Glu Ala Arg		
515	520	525
Leu Thr Ala Gln Cys Val Ala Glu Arg Phe Ser Glu Leu Glu His Leu		
530	535	540
Asp Arg Leu Ser Gly Arg Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp		
545	550	555
Gly Ser Leu Asn Thr Thr Lys		560
565		

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Leu Thr Gly Arg Val Gly Ser Gly Arg Phe Gly Asn Val Ser Arg Gly		
5	10	15
Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val Phe Asn Ala Ile Asp		
20	25	30
Glu Pro Ala Phe His Lys Glu Ile Glu Ile Phe Glu Thr Arg Met Leu		
35	40	45
Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser Asp Arg Val Asp Thr		
50	55	60
Gly Phe Val Thr Glu Leu Trp Leu Val Ile Glu Tyr His Pro Ser Gly		
65	70	75
Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val Asn Ile Glu Thr Tyr		80

